

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 14:56:27 ; Search time 14 Seconds
(without alignments)
1679.791 Million cell updates/sec

Title: US-08-813-323b-1

Perfect score: 2994
Sequence: 1 MESSKMDAAGTLQNPPLK.....IKDDTIFIKYVDTSLPDP 567

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2994	100.0	567	1 TRA3_MOUSE	Q06803 mus musculu
2	2886.5	96.4	567	1 TRA3_HUMAN	Q13114 homo sapien
3	837.5	28.0	501	1 TRA2_MOUSE	P39429 mus musculu
4	745.5	24.9	501	1 TRA2_HUMAN	Q12933 homo sapien
5	641.5	21.4	416	1 TRA1_MOUSE	Q13077 homo sapien
6	640	21.4	409	1 TRA1_MOUSE	P39428 mus musculu
7	209	7.0	458	1 DG17_DICD1	P11467 dictyosteli
8	168	5.6	1816	1 LMA4_MOUSE	P97927 mus musculu
9	164	5.5	919	1 RA50_AERPE	Q9YFZ1 aeropyrum p
10	161	5.4	634	1 MYSC_CHICK	Q61510 mus musculu
11	157.5	5.3	1102	1 MYSC_CHICK	P29616 gallus gall
12	151.5	5.1	704	1 MEPA_MOUSE	Q61847 mus musculu
13	149	5.0	1957	1 YDB6_SCHPO	Q10411 schizosach
14	147	4.9	1816	1 LMA4_HUMAN	Q16363 homo sapien
15	147	4.9	2230	1 GOG4_HUMAN	Q13439 homo sapien
16	147	4.9	3210	1 CEN6_HUMAN	P49454 homo sapien
17	146	4.9	1679	1 Y109_YEAST	P40457 saccharomyc
18	146	4.9	1727	1 ALM1_SCHPO	Q9UKX5 schizosach
19	145.5	4.9	944	1 NUP1_YEAST	P33280 saccharomyc
20	145	4.8	624	1 A33_PLEWA	Q02084 pleurodeles
21	145	4.8	1005	1 RA50_METJA	Q58718 methanococ
22	144.5	4.8	425	1 TM31_HUMAN	Q9BZY9 homo sapien
23	144	4.8	1935	1 MYH7_RAT	P02564 rattus norv
24	142.5	4.8	794	1 HMMR_MOUSE	Q00547 mus musculu
25	142.5	4.8	1940	1 MYH3_RAT	P12843 rattus norv
26	141.5	4.7	1935	1 MYH7_HUMAN	P02865 gallus gall
27	141	4.7	1940	1 MYH3_CHICK	P02930 archaeoglob
28	140.5	4.7	886	1 RA50_ARCFU	P13340 mesocricetu
29	140.5	4.7	1934	1 MYH7_MESAU	Q58687 pyrococcus
30	140	4.7	879	1 RA50_PYROH	P11055 homo sapien
31	139.5	4.7	1940	1 MYH3_HUMAN	P25186 saccharomyc
32	139	4.6	1790	1 USO1_YEAST	Q9UKX3 homo sapien
33	139	4.6	1938	1 MYH3_HUMAN	

34	138.5	4.6	886	1 RA50_SULAC	O33600 sulfolobus
35	137	4.6	1046	1 SBCC_LACLA	Q9CFZ0 lactococcus
36	137	4.6	1935	1 MYSC_CYPRA	O90339 cyprinus ca
37	136.5	4.6	551	1 RN27_MOUSE	O99P12 mus musculu
38	136.5	4.6	1935	1 MYH7_PIG	P79293 sus scrofa
39	136.5	4.6	1939	1 MYH6_HUMAN	P13533 homo sapien
40	136	4.5	704	1 MEPA_RAT	P28826 rattus norv
41	136	4.5	1941	1 MYH2_HUMAN	Q9UKX2 homo sapien
42	135	4.5	390	1 TPT1_BOVIN	P27628 bos taurus
43	133.5	4.5	852	1 RA50_THEMA	O9X1X1 thermotoga
44	133.5	4.5	999	1 CARP_MOUSE	O99KFT mus musculu
45	133.5	4.5	1084	1 MYSS_RABIT	P02562 oryctolagus

ALIGNMENTS

RESULT 1
TRA3_MOUSE STANDARD; PRT; 567 AA.
ID TRA3_MOUSE
AC Q06803: 062380:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TNF receptor associated factor 3 (CD40 receptor associated factor 1)
DE (CRAFT) (TRAFAFMN).
GN TRAF3 OR CRAFT OR TRAFAMN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_Taxid=10090;
RX MEDLINE=95144010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAFT, a relative of TRAF, in CD40 signalling."; Science 267:1494-1498(1995).
RN [2]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=96299439; PubMed=8660894;
RA Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lonberg N.,
RA Dinulos M.B., Distche C.M., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Lacy E.;
RT "A candidate gene for the amniotless gastrulation stage mouse mutation encodes a TRAF-related protein."; Dev. Biol. 177:374-390(1996).
RL
CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR ASSOCIATED FACTORS (POTENTIAL).
CC -1- TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT FOUND IN LIVER.
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5, HIGHEST LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION, FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 MATH/TRAFF DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
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CC
CC EMBL: U21050; AAC52175.1; -
CC EMBL: U33840; AAC52710.1; -
CC MGD: MGI:108041; Traf3.

DR InterPro: IPR002083; MATH.
 DR InterPro: IPR003007; TRAF.
 DR InterPro: IPR001293; ZnF-TRAF.
 DR InterPro: IPR001841; ZnF-ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00917; MATH; 1.
 DR Pfam: PF02176; zf-TRAF; 2.
 DR SMART: SM00061; MATH; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR PROSITE: PS50145; ZF-TRAF; 2.
 DR Zinc-finger: Coiled coil; Repeat.
 KW Zinc-finger; Coiled coil; Repeat.
 FT ZN_FING 67 76 RING-TYPE.
 FT ZN_FING 134 189 TRAF-TYPE 1.
 FT ZN_FING 190 248 TRAF-TYPE 2.
 FT DOMAIN 266 337 COILED COIL (POTENTIAL).
 FT DOMAIN 417 502 MATH/TRAF.
 FT CONFLICT 72 73 CE -> WO (IN REF. 2).
 FT CONFLICT 390 390 T -> M (IN REF. 2).
 SQ SEQUENCE 567 AA; 64263 MW; 25228343841192DC CRC64;

Query Match 100.0%; Score 2994; DB 1; Length 567;
 Best Local Similarity 100.0%; Pred. No. 1.3e-172;
 Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSKMDAGTLPNPPLKLOPRGAGSVLPBEGGYKREKFKVTEDEKYEKRCRLVLC 60
 DB 1 MESSKMDAGTLPNPPLKLOPRGAGSVLPBEGGYKREKFKVTEDEKYEKRCRLVLC 60
 QY 61 NKQTECGHRCFECSCMAALLSSSSPKCTACQESITIKDKVFNCKCKRELLAQVYCRNEG 120
 DB 61 NKQTECGHRCFECSCMAALLSSSSPKCTACQESITIKDKVFNCKCKRELLAQVYCRNEG 120
 QY 121 RCGAEOLTLGHLVHLKNECCFEELPCRLADCKEVLKDLRDHYEKCKREATCSCK 180
 DB 121 RCGAEOLTLGHLVHLKNECCFEELPCRLADCKEVLKDLRDHYEKCKREATCSCK 180
 QY 181 SOVPMIKLQKHEDTDCPCVWVSCPHKCSVQTLRLSELSAHLSSECVNAPSTCSFKRYGVF 240
 DB 181 SOVPMIKLQKHEDTDCPCVWVSCPHKCSVQTLRLSELSAHLSSECVNAPSTCSFKRYGVF 240
 QY 181 SOVPMIKLQKHEDTDCPCVWVSCPHKCSVQTLRLSELSAHLSSECVNAPSTCSFKRYGVF 240
 DB 181 SOVPMIKLQKHEDTDCPCVWVSCPHKCSVQTLRLSELSAHLSSECVNAPSTCSFKRYGVF 240
 QY 241 OGTOQIATHESSAVQVHNLKESNSLEKVVSLQNESEYKKNSTIGSLHNOJCSFEIE 300
 DB 241 OGTOQIATHESSAVQVHNLKESNSLEKVVSLQNESEYKKNSTIGSLHNOJCSFEIE 300
 QY 301 IEROKEMLRNNESEKLIHLQVYIDSOAEKLEDEIRPEFRONWEEADSMKSSVESLQNRV 360
 DB 301 IEROKEMLRNNESEKLIHLQVYIDSOAEKLEDEIRPEFRONWEEADSMKSSVESLQNRV 360
 QY 361 TELESVDKSAGQAARNTGLLESQLSRHDQTLVSHDIRLADMDLRFQVLETASYNGVLIWK 420
 DB 361 TELESVDKSAGQAARNTGLLESQLSRHDQTLVSHDIRLADMDLRFQVLETASYNGVLIWK 420
 QY 421 IRDYKRRQEAVMGKTLSLSQPYTGYFGYKMCARVYLNDGNGKSTHLSLFFVIMRGE 480
 DB 421 IRDYKRRQEAVMGKTLSLSQPYTGYFGYKMCARVYLNDGNGKSTHLSLFFVIMRGE 480
 QY 421 IRDYKRRQEAVMGKTLSLSQPYTGYFGYKMCARVYLNDGNGKSTHLSLFFVIMRGE 480
 DB 421 IRDYKRRQEAVMGKTLSLSQPYTGYFGYKMCARVYLNDGNGKSTHLSLFFVIMRGE 480
 QY 481 YDALPMPFKOKVTLMLMDQSSRRHGDFAKPPDNSSSRKPKPGEMNINASGCVFAQOT 540
 DB 481 YDALPMPFKOKVTLMLMDQSSRRHGDFAKPPDNSSSRKPKPGEMNINASGCVFAQOT 540
 QY 541 VLENGYIKDDTIFIKYIVDTSDLPDP 567
 DB 541 VLENGYIKDDTIFIKYIVDTSDLPDP 567

RESULT 2
 TRAF3_HUMAN STANDARD; PRT; 568 AA.
 AC Q13114; Q13076; Q13947; Q12990;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE 15-TUN-2002 (Rel. 41, Last annotation update)
 DE TNF receptor associated factor 3 (CD40 receptor associated factor 1)
 DE (CRAFT) (CD40 binding protein) (CD40BP) (LMP1 associated protein)
 DE (LMP1) (CAP-1).
 GN TRAF3 OR CRAFT OR CAP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95184010; PubMed=7533327;
 RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
 RT "Involvement of CRAFT, a relative of TRAF, in CD40 signalling.";
 RL Science 267:1494-1498(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=95163092; PubMed=7859281;
 RA Mosialos G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C.,
 RA Kieff E.;
 RT "The Epstein-Barr virus transforming protein LMP1 engages signaling
 RT proteins for the tumor necrosis factor receptor family.";
 RL Cell 80:389-399(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Fetal brain;
 RX MEDLINE=95129692; PubMed=7530216;
 RA Sato T., Irie S., Reed J.C.;
 RT "A novel member of the TRAF family of putative signal transducing
 RT proteins binds to the cytosolic domain of CD40.";
 RL FIBS Lett. 358:113-118(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95073988; PubMed=7527023;
 RA Hu H.M., O'Rourke K., Boguski M.S., Dixit V.M.;
 RT "A novel RING finger protein interacts with the cytoplasmic domain of
 RT CD40.";
 RL J. Biol. Chem. 269:30069-30072(1994).
 CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
 CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
 CC ASSOCIATED FACTORS (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
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 CC -----
 DR EMBL: U01092; AAC50112.1; -
 DR EMBL: U19260; AAA65732.1; -
 DR EMBL: U38509; AAA68195.1; -
 DR EMBL: U15637; AAA6753.1; -
 DR GeneW: HGNC:12033; TRAF3.
 DR MIM: 601896; -
 DR InterPro: IPR002083; MATH.
 DR InterPro: IPR003007; TRAF.
 DR InterPro: IPR001293; ZnF-TRAF.
 DR InterPro: IPR001841; ZnF-ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00917; MATH; 1.
 DR Pfam: PF02176; zf-TRAF; 2.
 DR SMART: SM00061; MATH; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.

```

RP SEQUENCE FROM N.A. Pubmed-8069916;
RX MEDLINE-94349371;
RA Roth M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kda tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
CC - FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
CC ACTIVATES NF-KAPPA-B.
CC - SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
CC HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
CC PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS
CC FACTOR RECEPTOR 2 (TNFR2).
CC - SUBCELLULAR LOCATION: Cytoplasmic.
CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC - SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.
CC - SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
CC -----
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CC or send an email to license@sdb.sdb.ch).
CC -----
CC EMBL: L35303; AAC37662.1; -.
CC DR HSSP; P12351; 1HW.
CC DR MGD; MGI:101835; Traf2.
CC DR InterPro; IPR002083; MATH.
CC DR InterPro; IPR003007; TRAF.
CC DR InterPro; IPR001293; Znf.TRAF.
CC DR InterPro; IPR001841; Znf.ring.
CC DR Pfam; PF00097; zf-C3HC4; 1.
CC DR Pfam; PF00917; MATH; 1.
CC DR Pfam; PF02176; zf-TRAF; 2.
CC DR SMART; SM00061; MATH; 1.
CC DR SMART; SM00184; RING; 1.
CC DR PROSITE; PS00518; ZF_RING_1; 1.
CC DR PROSITE; PS00518; ZF_RING_2; 1.
CC DR PROSITE; PS0145; ZF-TRAF; 2.
CC KW Zinc-finger; Coiled coil; Repeat.
CC FT ZN_FING 34 73 RING-TYPE.
CC FT ZN_FING 124 180 TRAF-TYPE 1.
CC FT ZN_FING 177 233 TRAF-TYPE 2.
CC FT DOMAIN 298 348 COILED COIL (POTENTIAL).
CC FT DOMAIN 334 501 MATH/TRAF.
CC SQ SEQUENCE 501 AA; 56026 MW; 043B391180365F10 CRC64;
CC -----
Query Match 28.0%; Score 837.5; DB 1: Length 501;
Best Local Similarity 33.5%; Pred. No. 2,3e+43;
Matches 194; Conservative 88; Mismatches 196; Indels 99; Gaps 16;
DB 1 MAAASVTSFGSLELDF-----GFSKTLGTFLBAKYLCSAKNNILRRPFOA 47
OY 7 MDAATLDPNPRLIPDPRGAGSVLVEQGGYKEKFPVT-VEDKYKSEKRLVLCNPKOT 65
DB 1 MAAASVTSFGSLELDF-----GFSKTLGTFLBAKYLCSAKNNILRRPFOA 47
OY 66 ECGHPRFESMAALLISSSPKCTAC-----QSTI---KDKVFNDNCRRKELLALQVC 116
DB 48 OCGHRCFSFCILTSILSGPNCACAYEGLYEIGSILLESSAFPDNARREVESLRVVC 107
OY 117 RNDGGCAEOLTLGHLYLHNEQGFELPCLRADCKEVLRLKRDJHVEACSKYREATC 176
DB 108 PND--GCTWKGTLKTESCHSGCLRPILLTSC--PAGKGLVRLSEKNNHTEDQCPRLASC 163
OY 177 SHKSGVPMIKLQKHEDTDCPVVVSQPRKCSVQTLRLSELNHLSECVNAPSTCSFRY 236
DB 164 QHCRAPCSHVDELYHEY-CEKPLTC-DGCGKKKIPREFODHVRACSKCVRILRFHTV 221
OY 237 GCYFQSTNQIKAHASSAVOHVNLWLEMSNLSKEKVS-----LLQNESVEKRS 286
DB 222 GCSEWETENLQDHELQRLREHLAL--LSSFLDAQSPQTLNQVGRPELLQCOQLLEOK- 278

```


TNF receptor associated factor 1 (TRAF1) (Epstein-Barr virus-induced protein 6).

DE TRAF1 OR EB16.

GN Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RM [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphoma;

RA MEDLINE=95163092; PubMed=7859281;

RA Mosialos G., Birkenbach M., Yalamanchili R., VandeWade T., Ware C., Kleif E.;

RA "The Epstein-Barr virus transforming protein Lmp1 engages signaling proteins for the tumor necrosis factor receptor family.";

RT Cell 80:389-399(1995).

RL -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).

CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS HETERODIMER CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.

CC -----

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CC -----

CC EMBL: U19261; AAA62309.1; -

CC Genew: HGNC:12031; TRAF1.

DR MIM: 601711; -

DR InterPro: IPR002083; MATH.

DR InterPro: IPR003007; TRAF.

DR Pfam: PF00917; MATH; 1.

DR SMART: SM00061; MATH; 1.

KW Coiled coil.

FT DOMAIN 182 264 COILED COIL (POTENTIAL).

FT DOMAIN 269 354 MATH/TRAF.

FT SEQUENCE 416 AA; 46163 MW; A956A123A40D284A CRC64;

SO

Query Match 21.4%; Score 641.5; DB 1; Length 416;

Best Local Similarity 35.5%; Pred. No. 1e-31;

Matches 165; Conservative 71; Mismatches 126; Indels 103; Gaps 17;

QY 137 KNECOFEELPCLRADCKEYLRKLDLHVEKACKYREATCSHCKSQVPMIKLQKHEDTDC 196

DB 15 ENEPFPCPTVCCDPRKPP-----RALCCACACSENP-----RNEDGIC 54

QY 197 PCVVVSCPHKCSYQTL-----LRSELNAHLSECVNAPSTCSFKRYGCVFOGTNOQIAK 248

DB 55 P-----KCRGDIQSTISPGSRILRTQKKAH-PEVAEAGICCPAGVCSFKSGSPQSQ 105

QY 249 AHEASSAVQVNL-----KMS-----NSLEKVSILQ--NESVEKKSTIO-SLH 291

DB 106 EHEVTQSHTSHLNLGFMKQMKARLCCGLSGPMALQLEMLSDQLQAAAEVAGDLEVDY 165

QY 292 NQICSEFIERQKEMLRNNEKSLHLQRYIDSQAELKELDKETIRPFRRNNEADSKMS 351

DB 166 RAPPS-----ESQEE-----LALQHM--KEKRLAELBEGLKLVF-----E 198

QY 352 SVESLQNRVTELESVDKSAQAAARNTGLLESQLSRH-----DOTLSVHDIRLA 399

DB 199 NIVAVLAKKEVE-----ASHLALATSIHQSDLRERITLSLEQRVLELOOTLAQKQALG 251

QY 400 DMDLRPOVLEASVNGVLIKIRIDYKRRKQEAIVGKLTLSYQPFYTGFGYKMCARVYL 459

DB 252 KLEOSLRIMEBASFDGIFLAKITVTRKCHESACGRVLSLFPAPFTATAYGKLCRLVYL 311

QY 460 NGDGMKGTHLSLFYIMRGEYDALLPMPFKOKVTILMDQSGSSRRHLDGAKFPDPNSS 519

DB 312 NGDGTGRTHLSLFYIMRGEYDALLPMPFKOKVTILMDQ--NNRHALDARPDLSAS 370

QY 520 FKRPTEGMNIAAGCPVEVAQTVLEN--GYIKDITFIYIVYDTS 562

DB 371 FQRQSEFNVAAGCPLEFFPLSKQSPKHAHVKDDTFLKCIYETS 415

RESULT 6

TRAF_MOUSE STANDARD; PRT; 409 AA.

ID TRAF_MOUSE

AC P39428;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE TNF receptor associated factor 1 (TRAF1).

GN TRAF1.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RM [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 123-135 AND 390-402.

RA MEDLINE=94349371; PubMed=8069916;

RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;

RT "A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";

RL Cell 78:661-692(1994).

CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). THIS HETERODIMER CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.

CC -----

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CC -----

CC EMBL: L35302; AAC37663.1; -

CC GDB: MGI:101836; Traf1.

DR InterPro: IPR002083; MATH.

DR InterPro: IPR003007; TRAF.

DR Pfam: PF00917; MATH; 1.

DR SMART: SM00061; MATH; 1.

KW Coiled coil.

FT DOMAIN 167 256 COILED COIL (POTENTIAL).

FT DOMAIN 262 347 MATH/TRAF.

FT SEQUENCE 409 AA; 45464 MW; EBA7FEE5639FEDDF CRC64;

SO

Query Match 21.4%; Score 640; DB 1; Length 409;

Best Local Similarity 35.5%; Pred. No. 1.3e-31;

Matches 162; Conservative 72; Mismatches 136; Indels 86; Gaps 15;

QY 137 KNECOFEELPCLRADCKEYLRKLDLHVEKACKYREATCSHCKSQVPMIKLQKHEDTDC 196

DB 9 ENEPF-----GCPAPPCD-----PSEPVLCCTCAE-----NLKDEEDNIC 48

QY 197 PCVVVSCPHKCSYQTLRLSELNAHLSECVNAPSTCSFKRYGCVFOGTNOQIAHEASSAV 256

DB 49 PKCADNLLHVHSPGSLTQE-KVH-SDVAEAEITMCPAGVCSFKSGSPSMQHEATQS 106

QY 257 QHVNL-----LKMSNS-----LEKVSILLQNEVEKNSIQSLHNGICSEFIEI 301

DB 107 SHYLLAVLKEMKSSPGNLSGAPMALERNLSLQ-----LQAAVEATGDLVDY 157

Query Match	7.0%	Score 209;	DB 1;	Length 458;
Best Local Similarity	20.3%;	Pred. No. 1e-05;		
Matches 115; Conservative	80;	Mismatches 177;	Indels 194;	Gaps 27;

RESULT	8	LM4_MOUSE	LM4_MOUSE	STANDARD:	PRT;	1816	AA.
ID	LM4_MOUSE						
AC	P97927; P70409; 088785;						
DT	15-JUN-2002 (Rel. 41, Created)						
DT	15-JUN-2002 (Rel. 41, Last sequence update)						
DT	15-JUN-2002 (Rel. 41, Last annotation update)						
DE	Laminin alpha-4 chain precursor.						
GN	LAMA4.						
OS	Mus musculus (Mouse).						
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX	NCBI_TaxId=10090;						
RN	[1]						
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 462-469; 478-483; 776-782 AND 940-945.						
RC	STRAIN=BA6/c; TISSUE=Endothelial cells;						
RX	MEDLINE=97365207; PubMed=9219532;						
RA	Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,						
RA	Sorokin L.M.;						
RT	"Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of						
RTL	endothelium";						
RTL	Eur. J. Biochem. 246:727-735(1997).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Heart;						
RX	MEDLINE=97202462; PubMed=9049981;						
RA	Liu J., Mayne R.;						
RA	"The complete cDNA coding sequence and tissue-specific expression of						
RT	the mouse laminin alpha 4 chain."						
RTL	Matrix Biol. 15:433-437(1996).						

[3]
SEQUENCE FROM N.A.
RC STRAIN-BALB/C.
MEDLINE=98010627; PubMed=9346933;
RA Iivanainen A., Kortasmaa J., Sahberg C., Morita T., Bergmann U.,
Thelieff I., Tryggvason K.;
"Primary structure, developmental expression, and immunolocalization
of the murine laminin alpha4 chain."
J. Biol. Chem. 272:27862-27868(1997).
[4]
SEQUENCE OF 836-1106 FROM N.A.
RC STRAIN-ICR: TISSUE-Placenta;
MEDLINE=97296337; PubMed=9151674;
RA Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
Jenkins N.A., Copeland N.G., Saes J.R.;
"The laminin alpha chains: expression, developmental transitions, and
chromosomal locations of alpha-5, identification of heterotrimeric
laminins 8-11, and cloning of a novel alpha3 isoform."
J. Cell Biol. 137:685-702(1997).
[5]
SEQUENCE OF 1467-1691 FROM N.A.
RC TISSUE-Placenta;
MEDLINE=97187457; PubMed=9034910;
RA Lentz S.I., Miner J.H., Saes J.R., Snider W.D.;
"Distribution of the ten known laminin chains in the pathways and
targets of developing sensory axons."
J. Comp. Neurol. 378:547-561(1997).
-1- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration, and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
-1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
comprising one long and three short arms with globules at each
end.
-1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
MEMBRANES (MAJOR COMPONENT).
-1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PERIPHERAL NERVES,
CARDIAC MUSCLE, FAT, DERMIS, LUNG STROMA, AORTIC ENDOTHELIUM,
ENDOCARDIUM AND ENDOTHELIDUM OF BLOOD VESSELS IN SKIN AND BRAIN.
-1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
-1- DOMAIN: DOMAIN G IS GLOBULAR.
-1- SIMILARITY: CONTAINS 3.5 LAMININ EGF-LIKE DOMAINS.
-1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U58950; AAB41840.1; -
DR EMBL: Y09827; CA70970.1; -
DR EMBL: U59865; AAC24725.1; -
DR EMBL: U88352; AAC53178.1; -
DR HSSP: U69176; AAC52982.1; -
DR HSSP: P02468; IKLO.
DR MGD: MGI.109321; Lama4.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR Pfam: PF00053; Laminin_EGF; 3.
DR Pfam: PF00054; Laminin_G; 4.
DR SMART: SM00181; EGF; 3.
DR PROSITE: PS00022; EGF_1; UNKNOWN.1.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; 3.
DR PROSITE: PS00025; LAM_G_DOMAIN; 5.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	1816	LAMININ ALPHA-4 CHAIN.
FT	DOMAIN	82	131	LAMININ EGF-LIKE 1.
FT	DOMAIN	132	186	LAMININ EGF-LIKE 2.
FT	DOMAIN	187	240	LAMININ EGF-LIKE 3.
FT	DOMAIN	241	255	LAMININ EGF-LIKE 4 (INCOMPLETE).
FT	DOMAIN	256	825	DOMAIN II AND I.
FT	DOMAIN	826	1030	LAMININ G-LIKE 1.
FT	DOMAIN	1042	1222	LAMININ G-LIKE 2.
FT	DOMAIN	1229	1397	LAMININ G-LIKE 3.
FT	DOMAIN	1462	1633	LAMININ G-LIKE 4.
FT	DOMAIN	1640	1813	LAMININ G-LIKE 5.
FT	DOMAIN	431	523	COILED COIL (POTENTIAL).
FT	DOMAIN	556	604	COILED COIL (POTENTIAL).
FT	DOMAIN	655	717	COILED COIL (POTENTIAL).
FT	DOMAIN	770	799	COILED COIL (POTENTIAL).
FT	STATE	717	719	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	82	91	BY SIMILARITY.
FT	DISULFID	84	98	BY SIMILARITY.
FT	DISULFID	101	110	BY SIMILARITY.
FT	DISULFID	113	129	BY SIMILARITY.
FT	DISULFID	132	146	BY SIMILARITY.
FT	DISULFID	134	155	BY SIMILARITY.
FT	DISULFID	157	166	BY SIMILARITY.
FT	DISULFID	169	184	BY SIMILARITY.
FT	DISULFID	187	202	BY SIMILARITY.
FT	DISULFID	189	209	BY SIMILARITY.
FT	DISULFID	212	221	BY SIMILARITY.
FT	DISULFID	224	238	BY SIMILARITY.
FT	DISULFID	266	266	INTERCHAIN (PROBABLE).
FT	DISULFID	269	269	INTERCHAIN (PROBABLE).
FT	CARBOHYD	104	104	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	215	215	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	308	308	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	333	333	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	550	550	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	571	571	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	574	574	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	639	639	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	735	735	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	751	751	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	754	754	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	780	780	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	803	803	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1088	1088	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1261	1283	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1361	1361	N-LINKED (GLCNAC. . .)
FT	CONFLICT	8	8	C -> S (IN REF. 2).
FT	CONFLICT	18	18	C -> Y (IN REF. 2).
FT	CONFLICT	248	248	G -> R (IN REF. 3).
FT	CONFLICT	297	297	G -> A (IN REF. 3).
FT	CONFLICT	431	433	THR -> HPS (IN REF. 2).
FT	CONFLICT	679	679	S -> C (IN REF. 3).
FT	CONFLICT	703	703	D -> G (IN REF. 2).
FT	CONFLICT	706	706	N -> H (IN REF. 2).
FT	CONFLICT	728	728	K -> R (IN REF. 2).
FT	CONFLICT	730	730	F -> I (IN REF. 2).
FT	CONFLICT	779	779	R -> G (IN REF. 1).
FT	CONFLICT	810	810	R -> S (IN REF. 3).
FT	CONFLICT	865	867	AEP -> QT (IN REF. 2).
FT	CONFLICT	936	936	K -> E (IN REF. 3).
FT	CONFLICT	970	970	L -> V (IN REF. 3).
FT	CONFLICT	1132	1132	H -> R (IN REF. 2).
FT	CONFLICT	1200	1200	F -> I (IN REF. 2).
FT	CONFLICT	1382	1382	D -> A (IN REF. 2).
FT	CONFLICT	1413	1414	NS -> EF (IN REF. 1).
FT	CONFLICT	1489	1489	A -> S (IN REF. 2).
SO	SEQUENCE	1816	201818	MW: B49C45F3A4599D8 CRC64:

Query Match
Best Local Similarity5.6%; Score 168; DB 1; Length 1816;
19.6%; Pred. No. 0.014;

```

Matches 105; Conservative 79; Mismatches 201; Indels 152; Gaps 24;

QY 2 ESSKKMDAGTLPDPNPLKLPDRGAGSVLPVPGGKKEKFEVTVEDKYCEKCRVLGN 61
D 46 DPSTSSGVTTLGRPLPAERCDG-----FFPTLGG--ECAPCD--CN 85
QY 62 PKOTEC--GHRFESGMAALLSSSPKCAQESIIKDKV-----PRDNC----- 104
D 86 GNSHECLDGSFCLHQR---NTTGEHCEKCLDGYIGDSIRGPRRCQCPCLPHLANF 142
QY 105 ---CKRITLALQYCRNE--GRCAEQDITLGH---LVHLKNECPPELPCIRADCK-- 153
D 143 AESCYRNGAVRCICKEKENVYPC--BRCAPGYGNPLLI-----GSTCKKCCSGN 192
QY 154 ---EKVLKRLDRHVEKACK--YEATCSHCKSQVPMIKLQKHEDTDC-----PCVYV 201
D 193 SDNLIFEDC-DEITGOCRCNLANTGFCERCAPGYGDARAKKCAVNCGGGPGDSV 251
QY 202 SCPHKCSVOTLRLSELSAHLSECVNAPSTCSFKRYCGVGTNO-----OI 247
D 252 T--GEC-----LEEGFEVPTGCD---KCWMDLTDDLRLALSTIESKGL 292
QY 248 KAHESAVOHVNLKEMSNLSLEKYSLLQNESVEKNKSISLHNOICFETIEF----- 302
D 293 SVSSGAAHRHVTDMNSTIHLRLSERENQYTLKRIQINSENTELRSLDVEGLEK 352
QY 303 ---ROKEMLRNNS-----KILHLQRVIDSQAELKELDEKREPRNWE----- 344
D 353 GSOASRKMVLVEKESMDTIDQATHLVEQAHNMNRDKIQELNSKMLLYGGEOLGPERIAK 412
QY 345 ---EADMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLVSHDIRLAMD 402
D 413 LVLAQKLEBEIRSRPFLTHRELVEADEAQELLSQLANMORLHNDTSLPVLVEQD 472
QY 403 -----LRFQVLETSYNGVLIKIRDKR-----RKQAVMKETSL 439
D 473 DYNAKISLDQESINQALDHYRAEDMNRATITKQRDHKEHREKXEMEVGASLSM 529

RESULT 9
RA50_AERPE STANDARD; PRT; 919 AA.
ID RA50_AERPE
AC 09YFZ1:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA double-strand break repair rad50 Atpase.
GN RAD50 OR APE0110.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K1:
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Aikai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC CC
CC -!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC rad50/mre11 complex possesses single-strand endonuclease activity
CC and ATP-dependent double-strand-specific exonuclease activity.
CC Rad50 provides an ATP-dependent control of mre11 by unwinding
CC and/or repositioning DNA ends into the mre11 active site (By
CC similarity).
CC -!- SUBUNIT: Forms a complex with mre11 (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.

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CC
DR EMBL; AP000058; BAA79020.1;
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR003405; SMC_C.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF02463; SMC_N; 1.
DR Pfam; PF02483; SMC_C; 1.
KW DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
FT NP_BIND 31
FT DOMAIN 202 758 COILED COIL (POTENTIAL).
SQ SEQUENCE 919 AA; 104138 MW; 7BFAA80EB601B9DD CRC64;

Query Match 5.5%; Score 164; DB 1; Length 919;
Best Local Similarity 21.1%; Pred. No. 0.011;
Matches 98; Conservative 77; Mismatches 176; Indels 114; Gaps 16;

QY 25 RGAGSVLPEEGYKKEKFEVTVEDKYCEKCRVLGNPKQ--TECGHRFESGMAALLSS 82
D 358 REAEKRLLEARSSTIKERQRTLDYRTGRSIVTNRVLSCKR-----DLGGS 410
QY 83 SSPKCTACQ-ESIIKDKYFKDCKKREITLALQYCR-----NKGCAEQDITLGH 132
D 411 EKPESEVLERLDAVINDESKARALDOEASALEAEARLVQALSMLEBSGSAKCPVCG-- 468
QY 133 LVHLKNEQFELCLRDCKEXVLRLDRDHYEAKCKYRATCSHCKSQVPMIKLQKH 192
D 469 -----ALPPGRRAIARHYRHE-ARLRLKAKKEAAAEKARASRLQDDRRR 517
QY 193 DTDCPCVYVSCPHKCSVOTLRL--SELSAHLSECVNAPSTCSFKRYCGVGTNOQIKAH 250
D 518 -----IELLSRLNQLBEGLRE-----LGFOTEDBLAKAE 547
QY 251 EASSAV-OHVNLKEMSNLSLEKYSLLQNSV---EKNSIOSLHNOICFETIEROK 305
D 548 QKRLMRERLEELRLKLSNLSLEKYSRLNLSREVALREAKTALVELIQR---LGKKEEAR 603
QY 306 EMLNNESKILHLQRVIDSQAELK-----KEL---DKE 335
D 604 EKLTLSSESKKLEKRLVSAEDLATRLGITAYRSLDLEKAREALEGVCKELSAIERR 663
QY 336 IRPRNWEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLVSH 395
D 664 LEARRLKEBAKLMKEADQVMKRLBELLEAEKKLRKEVSRKSEIERLKEVQNTLAELD 723
QY 396 IRLAMDRLPROVLETFASYNGVLIKIRDKRROQEAVMGKTSLSY 440
D 724 DRISRIDREMGELQT-----RIREMKSRK--ASGEELAKLY 757

RESULT 10
2147_MOUSE STANDARD; PRT; 634 AA.
ID 2147_MOUSE
AC 061510;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Zinc finger protein 147 (Tripartite motif protein 25) (Estrogen
DE responsive finger protein) (Efp).
GN ZNF147 OR TRIM25 OR ZFP147 OR EFP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```


RC TISSUE-Uterus, Ovary, and Placenta;
 RA MEDLINE-96025835; PubMed-7592654;
 RX Orimo A., Inoue S., Ikeda K., Noji S., Muramatsu M.,
 RT "Molecular cloning, structure, and expression of mouse estrogen-
 responsive finger protein Efp. Co-localization with estrogen receptor
 RT mRNA in target organs.";
 RL J. Biol. Chem. 270:24406-24413(1995).
 CC -1- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
 CC -----
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 CC -----
 DR EMBL: D63902; BAA09941.1; -
 DR MGI: 102749; Trlm25.
 DR InterPro: IPR001870; Gamma_carboxylase.
 DR InterPro: IPR003878; SPRY_domain.
 DR InterPro: IPR003877; SPRY_receptor.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00622; SPRY; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00449; SPRY; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS00508; ZF_RING_2; 1.
 DR KZING: KZING; Coiled coil.
 FT 2N_FING 13 54 RING-TYPE.
 FT DOMAIN 215 305 COILED COIL (POTENTIAL).
 FT 514 631 SPRY.
 SQ SEQUENCE 634 AA; 71772 MW; 6659C9DE283E611 CRC64;
 Query Match 5.4%; Score 161; DB 1; Length 634;
 Best Local Similarity 18.5%; Pred. No. 0.011;
 Matches 75; Conservative 65; Mismatches 130; Indels 136; Gaps 17;
 QY 48 DKYCKCKRLVLCNPKOTCGHRCFSCMAALLSSSP--KCTACQESIIRKDYKFKDNC 105
 DB 9 EELSCSVCLLEFKPEYPTTCGHNFCSCLEDERVWVGPPYRCQGR-----KVYQ--V 59
 QY 106 KREILALQVYC-----RNEGRCGEQLTLGHLVHLK-NECQ 141
 DB 60 RPOLOKTVMCAVVEQFLAQEAARFPVDDMTTPPARFSASSATOVACDCLTEIAVKTG- 118
 QY 142 FEELPCIRADCKEKV-----LRKDLRDHVEKAC---KYREATCSHCKSQVP 184
 DB 119 ---LVCMASFCQELHRPHEDSPAFQHPLOSPRDLIRKCKTQHNLRREFP----- 168
 QY 185 MIKLQKHEDYDCPVVVSCHK-CSTVQTLRLSELNAHLECVNABSTCSFKRYGCVFOGT 243
 DB 169 -----EHQECICHCICLVEHKTCSPITL--SQASADL----- 197
 QY 244 NQOTKAHEASSAVOHVULKEWNSLEKYSLLQNSVEKNSIOSLHNOICSELEIER 303
 DB 198 -----EYKLRNKLTJTHSHINGATKALEVRSKQOCQVDSMKR 235
 QY 304 OKEMLRNNSKILHLOVID-----SQAEKLKELDKET-----RPRONMEADSMKS 351
 DB 236 KMEQIR---QEYMKKAVIDAETSRLRKEBEKRYNGKFDITIVLVKKKSEMQTKLA 292
 QY 352 SVESLQNVTELESVDKSA---GOAARNLTLLSQSLSRHDQTSVH 394
 DB 293 EVELIMDKGDEFLEKRAKLOGESTKPYIPIKIDLD-HDLINGIV 337

AC P29616;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Myosin heavy chain, cardiac muscle isoform (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 65-1102 FROM N.A.
 RC STRAIN-Broiler; Tissue-Heart;
 RX MEDLINE-92130260; PubMed-1774788;
 RA Stewart A.F.R., Camoretti-Mercado B., Perlman D., Gupta M.,
 RA Jakovic S., Zak R.;
 RT "Structural and phylogenetic analysis of the chicken ventricular
 RT myosin heavy chain rod.";
 RL J. Mol. Evol. 33:357-366(1991).
 RN [2]
 RP SEQUENCE OF 1-259.
 RC TISSUE-Heart;
 RX MEDLINE-93039740; PubMed-1418675;
 RA Watanabe B.;
 RT "Amino-acid sequence of the short subfragment-2 in adult chicken
 RT cardiac muscle myosin.";
 RL Biol. Chem. Hoppe-Seyler 373:1045-1054(1992).
 CC -1- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -1- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
 CC -1- TISSUE SPECIFICITY: VENTRICULAR MUSCLE AND TRACES LEVELS IN THE
 CC ATRIUM. ALSO TRANSIENT EXPRESSION IN SKELETAL MUSCLE DURING FETAL
 CC DEVELOPMENT AND REGENERATION FOLLOWING FREEZE INJURY.
 CC -1- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -1- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
 CC WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
 CC CONSERVED.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X59552; CAA42130.1; -
 DR HSSP: P03437; IHFM.
 DR InterPro: IPR002928; Myosin_tail.
 DR Pfam: PF01576; Myosin_tail; 1.
 KW Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding;
 KW ATP-binding; Multigene family.
 FT NON_TER 1
 FT DOMAIN <1 1102 COILED COIL (POTENTIAL).
 FT CONFLICT 65 65 A -> T (IN REF. 1).
 FT CONFLICT 92 92 V -> A (IN REF. 1).
 FT CONFLICT 113 114 CS -> A (IN REF. 1).
 FT CONFLICT 135 135 H -> Q (IN REF. 1).
 FT CONFLICT 185 185 T -> R (IN REF. 1).
 SQ SEQUENCE 1102 AA; 128008 MW; 229368D049825DC CRC64;
 Query Match 5.3%; Score 157.5; DB 1; Length 1102;
 Best Local Similarity 20.1%; Pred. No. 0.034;
 Matches 102; Conservative 85; Mismatches 184; Indels 137; Gaps 21;

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OY 14 QPAPPLKLPDRGASVLYPEGGYKEFKVYEDKYKCEKRYLNCNPKQTECHRCSE 73
DB 591 QEDMIDLEKANSAAASLDKRGF-DKIINPMKQKYESQAL-----EASOKER 641
OY 74 SCMAALSSSPKCTACQESIINDXFKNCKRELALQVYCRNKGCAQLTGLHL 133
DB 642 SLSTELFKLN---AYEEL-DHL---ETLKREKNLQ---BEISDLTNQISEGKN 688
OY 134 VH-----LKNCOFE-----ELPCLRADCKEYLRKD-- 160
DB 689 LHEIEKVKQVEQEKSEVQALAEARGALEHESKTIHQLELSQKADFEKTLKED 748
OY 161 ---LRBHEKACKYKATC-SHCKSVPMIKLQKHEDTDCPVVSCPH----- 205
DB 749 MONIRNQOQRTIDSLQSTLDSKRSNEAIRLKKMEGDLNEMETQLSHANRHAATKS 808
OY 206 KCSQVTLRSELS-----AHSECNAPSTCSFKRYGCVGTMOQKA----- 249
DB 809 ARBLQVQIK-ELQVQLDLGHLEDEKQVSDRRNN-LQSELEDRALLDQTERAK 866
OY 250 ---HEASSAVQHVNLKESNS-----LEKKSLLQNESEYKKNKSIOSLHNOICSP 299
DB 867 LAEHELLEATERVNLHTQNTSLINQKKLEGDISQONEVEESIQECRNNEQAKAKAIT 926
OY 300 EIEROKEMLRNNEKTLHQRYIDQAKELKEKLEIRPFONNEADSM-----KSSVE 354
DB 927 DAAMAAEELKKRQDTSAHLERKKMKEQITDLOKRL-----DEAQIALKGKKRQIQ 979
OY 355 SLQNRVTELES-----VDRSAGQAAANTGLLESQSRHDQTSYVDIFLAMDL 403
DB 980 KLESVRLELENELNLRNSDAQKARKFERIKELTYQSEDKKNLA---RMDULID 1035
OY 404 RQVQETASVNGVLIWKIRDKYRKROEA 431
DB 1036 KLQD-----KVSKYKHQAEFA 1051

RESULT 12
MEPB_MOUSE
ID MEPB_MOUSE STANDARD; PRT; 704 AA.
AC 061847;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Meprin A beta-subunit precursor (EC 3.4.24.18) (Endopeptidase-2).
GN MEPIB OR MEP-1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94012651; Pubmed=8407940;
RA Gorbea C.M., Marchand P., Jiang W., Copeland N.G., Gilbert D.J.,
RT "Cloning, expression, and chromosomal localization of the mouse
RT meprin beta subunit".
RL J. Biol. Chem. 268:21035-21043(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA').
RC TISSUE=Kidney;
RX MEDLINE=96147211; Pubmed=8567689;
RA Dietrich J.M., Bond J.S., Jiang W.;
RT "A novel meprin beta' mRNA in mouse embryonal and human colon
RT carcinoma cells.".
RL J. Biol. Chem. 271:2271-2278(1996).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of protein and peptide substrates
CC preferentially on carboxyl side of hydrophobic residues.
CC -1- COFACTOR: BINDS 1 ZINC ION.
CC -1- SUBUNIT: HETEROHEXAOMER OF TWO ALPHA AND TWO BETA SUBUNITS WHICH
CC IS FORMED BY THE NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED
CC HETERODIMERS.

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RL FEBS Lett. 365:183-188(1995).

RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart;
 RX MEDLINE=97454279; PubMed=9310354;
 RA Richards A.J., Lucarini C., Pope F.M.;
 RT "The structural organisation of LAMA4, the gene encoding laminin
 alpha4.";
 RL Eur. J. Biochem. 248:15-23(1997).
 RN (3)
 RP SEQUENCE OF 236-1816 FROM N.A.
 RC TISSUE-Heart;
 RX MEDLINE=95048381; PubMed=7959779;
 RA Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
 RA Pope F.M.;
 RT "Localization of the gene (LAMA4) to chromosome 6q21 and isolation of
 a partial cDNA encoding a variant laminin A chain.";
 RL Genomics 22:237-239(1994).
 RN (4)
 RP SEQUENCE OF 66-1816 FROM N.A.
 RA Tubby B.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 is thought to mediate the attachment, migration, and organization
 of cells into tissues during embryonic development by interacting
 with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 different polypeptide chains (alpha, beta, gamma), which are bound
 to each other by disulfide bonds into a cross-shaped molecule
 comprising one long and three short arms with globules at each
 end.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
 MEMBRANES (MAJOR COMPONENT).
 CC -1- TISSUE SPECIFICITY: IN ADULT, STRONG EXPRESSION IN HEART, LUNG,
 OVARY SMALL AND LARGE INTESTINES, PLACENTA, LIVER; WEAK OR NO
 EXPRESSION IN SKELETAL MUSCLE, KIDNEY, PANCREAS, TESTIS, PROSTATE,
 BRAIN. HIGH EXPRESSION IN PERIT LUNG AND KIDNEY. EXPRESSION IN
 FETAL AND MEMBRAN TISSUES IS OBSERVED IN CERTAIN MESENCHYMAL CELLS
 IN TISSUES SUCH AS SMOOTH MUSCLE AND DERMIS.
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -1- DOMAIN: DOMAIN G IS GLOBULAR.
 CC -1- SIMILARITY: CONTAINS 3.5 LAMININ G-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
 CC -1- CAUTION: GENE LAMA4 WAS FORMERLY CALLED LAMA3.
 CC
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 CC
 DR EMBL: S78569; AAB34635.1; -
 DR EMBL: X91171; CAA62596.1; -
 DR EMBL: Y14240; CAA74636.1; -
 DR EMBL: X76939; CAA54258.1; -
 DR EMBL: Z99289; CAB16553.1; -
 DR HSSP: P02468; IKIO.
 DR GeneW: HGNC:6484; LAMA4.
 DR MIM: 600133; -
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR001791; Laminin_G.
 DR Pfam: PF00053; Laminin_EGF; 6.
 DR Pfam: PF00054; Laminin_G; 6.
 DR SMART: SM00180; EGF_Lam; 3.
 DR SMART: SM00282; LamG; 5.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 3.
 DR PROSITE: PS50025; LAM_G_DOMAIN; 5.
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	1816	LAMININ ALPHA-4 CHAIN.
FT	DOMAIN	82	131	LAMININ EGF-LIKE 1.
FT	DOMAIN	132	186	LAMININ EGF-LIKE 2.
FT	DOMAIN	187	240	LAMININ EGF-LIKE 3.
FT	DOMAIN	241	255	LAMININ EGF-LIKE 4 (INCOMPLETE).
FT	DOMAIN	256	825	DOMAIN II AND I.
FT	DOMAIN	826	1028	LAMININ G-LIKE 1.
FT	DOMAIN	1040	1220	LAMININ G-LIKE 2.
FT	DOMAIN	1227	1395	LAMININ G-LIKE 3.
FT	DOMAIN	1462	1633	LAMININ G-LIKE 4.
FT	DOMAIN	1640	1813	LAMININ G-LIKE 5.
FT	DOMAIN	313	396	COILED COIL (POTENTIAL).
FT	DOMAIN	466	521	COILED COIL (POTENTIAL).
FT	DOMAIN	574	607	COILED COIL (POTENTIAL).
FT	DOMAIN	655	717	COILED COIL (POTENTIAL).
FT	DOMAIN	770	799	CELL ATTACHMENT SITE (POTENTIAL).
FT	SITE	717	719	BY SIMILARITY.
FT	DISULFID	82	91	BY SIMILARITY.
FT	DISULFID	84	98	BY SIMILARITY.
FT	DISULFID	101	110	BY SIMILARITY.
FT	DISULFID	113	129	BY SIMILARITY.
FT	DISULFID	132	146	BY SIMILARITY.
FT	DISULFID	134	155	BY SIMILARITY.
FT	DISULFID	157	166	BY SIMILARITY.
FT	DISULFID	169	184	BY SIMILARITY.
FT	DISULFID	187	202	BY SIMILARITY.
FT	DISULFID	189	209	BY SIMILARITY.
FT	DISULFID	212	221	BY SIMILARITY.
FT	DISULFID	224	238	BY SIMILARITY.
FT	DISULFID	266	266	INTERCHAIN (PROBABLE).
FT	DISULFID	269	269	INTERCHAIN (PROBABLE).
FT	CARBOHYD	104	104	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	215	215	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	308	308	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	524	524	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	550	550	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	571	571	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	574	574	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	639	639	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	735	735	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	751	751	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	754	754	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	780	780	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	803	803	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1086	1086	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1281	1281	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1359	1359	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1411	1411	N-LINKED (GLCNAC. . .)
FT	CONFLICT	143	143	A -> P (IN REF. 1).
FT	CONFLICT	178	178	L -> F (IN REF. 1).
FT	CONFLICT	265	265	G -> GMDPPTS (IN REF. 4).
FT	CONFLICT	276	276	D -> A (IN REF. 4).
FT	CONFLICT	491	491	Y -> H (IN REF. 2 AND 3).
FT	CONFLICT	1057	1057	T -> P (IN REF. 1).
FT	CONFLICT	1110	1112	SGR -> GGP (IN REF. 4).
FT	SEQUENCE	1816	201908	MM; 04E9AR37940FAAD CAC64;
QY	Query Match	4.98;	Score 147;	DB 1; Length 1816;
QY	Best Local Similarity	19.38;	Pred. No. 0.26;	
QY	Matches 100;	Conservative 81;	Mismatches 206;	Indels 132; Gaps 25;
QY	16	NPPLKLPDRGAGSVIVPEGGYKEKYEKKEKRLVLCNPKQDEB--GHFCE 73		
QY	46	DPPEISBP-RVALGRPLPAAEKCNAGFFHTLSG--ECVPCD--CNGNSNECLDGSQYV 99		
QY	74	SCMAALSSSPKCTACQESIIKDKV-----FKDNC-----CKRETLALQVY 115		
QY	100	HCQR---NTTGEHCEKELCDGTIGDSINGAPQFCPCPCPLPLANFAESCYRRKNGAVRCI 156		
QY	116	CRNCRG-----CAEQLTLGLHLVHLNKECFEELPLRADCK---EKVLRLDLRDHYE 166		

Db 603 KEITVAVKHKTELES-----KHQDALTWTEKIQYVKQOY 638

OY 445 YT 446

Db 639 QT 640

Search completed: December 19, 2002, 15:00:48
Job time : 19 secs